GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: July 1, 2003, 14:30:42 ; Search time 367 Seconds
(without alignments)
9314.805 Million cell updates/sec

Title: US-10-010-742-305
Perfect score: 1518
Sequence: 1 atggagccctcctggcttca.....ttgcaaaaaaagtttgctaa 1518

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1518	100.0	2015	24	AAD24015	Human drug metabol
2	1516.4	99.9	2020	24	ABK33550	cDNA encoding huma
3	1028.8	67.8	1586	22	AAD09946	Human drug metabol
4	671.2	44.2	2343	22	AAS21297	Human cDNA sequenc
5	671.2	44.2	2381	24	ABK63921	cDNA encoding huma
6	671.2	44.2	2416	22	AAD09941	Human drug metabol
7	658.2	43.4	2327	24	ABK52898	cDNA encoding huma
8	651	42.9	2356	22	AAI99563	Human expressed po
9	651	42.9	2356	22	ABA06504	Human cDNA SEQ ID
10	651	42.9	2356	22	AAS40801	cDNA encoding nove
11	651	42.9	2356	22	AAS28959	cDNA encoding for
12	651	42.9	2356	22	AAS29592	Human endocrine po
13	651	42.9	2356	22	AAS34859	cDNA encoding nove
14	576	37.9	1186	23	AAS70309	DNA encoding novel
15	539	35.5	940	21	AAC79474	cDNA sequence of h
16	539	35.5	940	24	ABK29018	Human breast tumou
17	528.8	34.8	2576	24	ABN95640	Gene #2138 used to
18	528.8	34.8	2576	24	ABK50069	DNA encoding human
19	528.8	34.8	2576	24	ABL68591	Kidney cancer rela
20	524	34.5	1872	24	ABK50070	DNA encoding human
c 21	521.2	34.3	535	22	AAL23934	Human breast cance
22	517.6	34.1	760	22	AAL22366	Human breast cance
c 23	511.8	33.7	535	22	AAL15081	Human breast cance
24	511.2	33.7	2116	24	ABK50068	DNA encoding mouse
25	504.8	33.3	2462	24	ABK63715	Rat sequence diffe
26	503.6	33.2	535	22	AAL21247	Human breast cance
27	496.4	32.7	526	22	AAL23827	Human breast cance
28	494.8	32.6	1763	24	ABN95112	Gene #1610 used to
29	494.8	32.6	1763	24	ABL68271	Kidney cancer rela
30	494.8	32.6	1763	24	ABL68599	Kidney cancer rela
31	494.8	32.6	1763	24	ABL68881	Kidney cancer rela
32	492.8	32.5	498	22	AAH55549	Human breast tumou
33	490.4	32.3	534	22	AAL22422	Human breast cance
34	489.8	32.3	933	20	AAX84201	DNA encoding human
35	489.8	32.3	933	21	AAC79430	cDNA sequence of h
36	489.8	32.3	933	24	ABK28974	Human breast tumou
37	484.6	31.9	4123	24	ABK50067	DNA encoding mouse
38	480.4	31.6	539	22	AAL12371	Human breast cance
39	478.2	31.5	535	22	AAL24015	Human breast cance
40	462.4	30.5	757	22	AAL24582	Human breast cance
41	456.2	30.1	658	22	AAL15738	Human breast cance
42	455.8	30.0	641	22	AAL13497	Human breast cance
43	422.8	27.9	463	22	AAL13553	Human breast cance
44	417	27.5	2084	24	ABL67800	Oesophagus cancer
45	409.2	27.0	491	22	AAL14974	Human breast cance

ALIGNMENTS

RESULT 1
AAD24015
ID AAD24015 standard; cDNA; 2015 BP.
XX
AC AAD24015;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human drug metabolising enzyme (DME)-10 cDNA.
XX
KW Human; drug metabolising enzyme; DME-10; autoimmune; inflammatory;
KW cell proliferative; developmental; endocrine; eye; metabolic; AIDS;
KW gastrointestinal disorder; liver disorder; cancer; arteriosclerosis;
KW adult respiratory distress syndrome; anaemia; epilepsy; hypothyroidism;
KW hypothalamus; pituitary; diabetes; hypogonadism; conjunctivitis;
KW glaucoma; cystic fibrosis; hypercholesterolaemia; gastritis;
KW peptic ulcer; hepatitis; gene therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 117..1634
FT /*tag= a
FT /product= "Drug metabolising enzyme-10"
FT sig_peptide 117..209
FT /*tag= b
FT mat_peptide 210..1631
FT /*tag= c
FT /product= "Mature drug metabolising enzyme-10"
XX
PN WO200190334-A2.
XX

PD 29-NOV-2001.
XX
PF 25-MAY-2001; 2001WO-US17150.
XX
PR 25-MAY-2000; 2000US-207901P.
PR 01-JUN-2000; 2000US-208983P.
PR 07-JUN-2000; 2000US-209861P.
PR 15-JUN-2000; 2000US-211825P.
PR 22-JUN-2000; 2000US-213744P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Yue H, Sanjanwala MS, Baughn MR, Gandhi AR, Ring HZ, Elliott V;
PI Walia NK, Yang J, Khan FA, Ramkumar J, Tang YT, Hafalia A, Lal P;
PI Nguyen DB, Yao MG, Lee EA, Tribouley CM, Patterson C, Lu Y;
PI Burford N, Ding L, Bruns CM, Kearney L, Reddy R;
XX
DR WPI; 2002-097650/13.
DR P-PSDB; AAE14447.
XX
PT New human drug metabolizing enzymes and polynucleotides encoding the
PT enzyme for diagnosing, preventing or treating cell proliferative,
PT autoimmune/inflammatory, endocrine, eye, metabolic and gastrointestinal
PT disorders -
XX
PS Claim 5; Page 155-156; 158pp; English.
XX
CC The present sequence is human drug metabolising enzyme (DME)-10 cDNA.
CC DME polypeptide, polynucleotide and modulators are useful for
CC diagnosis, treatment and prevention of autoimmune/inflammatory,
CC cell proliferative, developmental, endocrine, eye, metabolic,
CC and gastrointestinal disorders, including liver disorders.
CC The autoimmune/inflammatory disorders treatable include
CC AIDS, adult respiratory distress syndrome, Addison's disease,
CC allergies, anaemia, asthma, atherosclerosis, osteoporosis, autoimmune
CC haemolytic anaemia, autoimmune thyroiditis, Crohn's disease, atopic
CC dermatitis, diabetic mellitus, Graves' disease, glomerulonephritis,
CC rheumatoid arthritis, scleroderma, systemic lupus erythematosus,
CC systemic sclerosis, ulcerative colitis, haemodialysis and uveitis,
CC viral, bacterial, fungal, parasitic, protozoal, helminthic infections
CC and trauma, and cell proliferative disorders such as cancer, actinic
CC keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis,
CC hepatitis and psoriasis. Developmental disorders include anaemia, renal
CC tubular acidosis, epilepsy, hypothyroidism and cataract, and endocrine
CC disorders include disorders of hypothalamus and pituitary, disorders
CC associated with hypopituitarism, including sarcoidosis, diabetes
CC insipidus, hypogonadism, disorders associated with hypothyroidism
CC including goitre, acute thyroiditis, Graves' disease, disorders
CC associated with hyperparathyroidism, pancreatic disorders such as type I
CC or type II diabetes mellitus, disorders associated with adrenals such as
CC hyperplasia, Cushing's disease, endometriosis, infertility,
CC hypergonadal disorders, and gynaecomastia. Eye disorders include
CC conjunctivitis, keratitis, glaucoma and macular degeneration, and
CC metabolic disorders include diabetes, cystic fibrosis, goitre,
CC hypercholesterolaemia, hypoglycaemia, hyperlipidaemia, lysosomal storage
CC diseases, obesity, phenylketonuria and hypocalcaemia. Also the molecules
CC are useful for treating gastrointestinal disorders such as dysphagia,
CC gastritis, peptic ulcer, cholelithiasis, cirrhosis, hepatitis,
CC hyperbilirubinaemia, constipation, diarrhoea, jaundice, Wilson's disease,
CC thrombosis and hepatic tumours. The DME polypeptide is also useful for
CC screening its agonist or antagonist.
XX
SQ Sequence 2015 BP; 570 A; 487 C; 410 G; 548 T; 0 other;

Query Match 100.0%; Score 1518; DB 24; Length 2015;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAGCCCTCCTGGCTTCAGGAACTCATGGCTCACCCCTTCTTGCTGCTGATCCTCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
pb        117 ATGGAGCCCTCCTGGCTTCAGGAACTCATGGCTCACCCCTTCTTGCTGCTGATCCTCCTC 176

Qy         61 TGCATGTCTCTGCTGCTGTTTCAGGTAATCAGGTTGTACCAGAGGAGGAGATGGATGATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        177 TGCATGTCTCTGCTGCTGTTTCAGGTAATCAGGTTGTACCAGAGGAGGAGATGGATGATC 236

Qy        121 AGAGCCCTGCACCTGTTTCCTGCACCCCCTGCCCACTGGTTCTATGGCCACAAGGAGTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 AGAGCCCTGCACCTGTTTCCTGCACCCCCTGCCCACTGGTTCTATGGCCACAAGGAGTTT 296

Qy        181 TACCCAGTAAAGGAGTTTGAGGTGTATCATAAGCTGATGGAAAAATACCCATGTGCTGTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 TACCCAGTAAAGGAGTTTGAGGTGTATCATAAGCTGATGGAAAAATACCCATGTGCTGTT 356

Qy        241 CCCTTGTGGGTTGGACCCTTTACGATGTTCTTCAGTGTCCATGACCCAGACTATGCCAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 CCCTTGTGGGTTGGACCCTTTACGATGTTCTTCAGTGTCCATGACCCAGACTATGCCAAG 416

Qy        301 ATTCTCCTGAAAAGACAAGATCCCAAAAGTGCTGTTAGCCACAAAATCCTTGAATCCTGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 ATTCTCCTGAAAAGACAAGATCCCAAAAGTGCTGTTAGCCACAAAATCCTTGAATCCTGG 476

Qy        361 GTTGGTCGAGGACTTGTGACCCTGGATGGTTCTAAATGGAAAAAGCACCGCCAGATTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 GTTGGTCGAGGACTTGTGACCCTGGATGGTTCTAAATGGAAAAAGCACCGCCAGATTGTG 536

Qy        421 AAACCTGGCTTCAACATCAGCATTCTGAAAATATTCATCACCATGATGTCTGAGAGTGTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 AAACCTGGCTTCAACATCAGCATTCTGAAAATATTCATCACCATGATGTCTGAGAGTGTT 596

Qy        481 CGGATGATGCTGAACAAATGGGAGGAACGCATTGCCCAAAACTCACGTCTGGAGCTCTTT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        597 CGGATGATGCTGAACAAATGGGAGGAACGCATTGCCCAAAACTCACGTCTGGAGCTCTTT 656

Qy        541 CAACATGTCTCCCTGATGACCCTGGACAGCATCATGAAGTGTGCCTTCAGCCACCAGGGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        657 CAACATGTCTCCCTGATGACCCTGGACAGCATCATGAAGTGTGCCTTCAGCCACCAGGGC 716

Qy        601 AGCATCCAGTTGGACAGTACCCTGGACTCATACCTGAAAGCAGTGTTCAACCTTAGCAAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        717 AGCATCCAGTTGGACAGTACCCTGGACTCATACCTGAAAGCAGTGTTCAACCTTAGCAAA 776

Qy        661 ATCTCCAACCAGCGCATGAACAATTTTCTACATCACAACGACCTGGTTTTCAAATTCAGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        777 ATCTCCAACCAGCGCATGAACAATTTTCTACATCACAACGACCTGGTTTTCAAATTCAGC 836

Qy        721 TCTCAAGGCCAAATCTTTTCTAAATTTAACCAAGAACTTCATCAGTTCACAGAGAAAGTA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        837 TCTCAAGGCCAAATCTTTTCTAAATTTAACCAAGAACTTCATCAGTTCACAGAGAAAGTA 896

Qy        781 ATCCAGGACCGGAAGGAGTCTCTTAAGGATAAGCTAAAACAAGATACTACTCAGAAAAGG 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        897 ATCCAGGACCGGAAGGAGTCTCTTAAGGATAAGCTAAAACAAGATACTACTCAGAAAAGG 956

Qy        841 CGCTGGGATTTTCTGGACATACTTTTGAGTGCCAAAAGCGAAAACACCAAAGATTTCTCT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        957 CGCTGGGATTTTCTGGACATACTTTTGAGTGCCAAAAGCGAAAACACCAAAGATTTCTCT 1016

Qy        901 GAAGCAGATCTCCAGGCTGAAGTGAAAACGTTCATGTTTGCAGGACATGACACCACATCC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1017 GAAGCAGATCTCCAGGCTGAAGTGAAAACGTTCATGTTTGCAGGACATGACACCACATCC 1076

Qy        961 AGTGCTATCTCCTGGATCCTTTACTGCTTGGCAAAGTACCCTGAGCATCAGCAGAGATGC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1077 AGTGCTATCTCCTGGATCCTTTACTGCTTGGCAAAGTACCCTGAGCATCAGCAGAGATGC 1136

Qy       1021 CGAGATGAAATCAGGGAACTCCTAGGGGATGGGTCTTCTATTACCTGGGAACACCTGAGC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1137 CGAGATGAAATCAGGGAACTCCTAGGGGATGGGTCTTCTATTACCTGGGAACACCTGAGC 1196

Qy       1081 CAGATGCCTTACACCACGATGTGCATCAAGGAATGCCTCCGCCTCTACGCACCGGTAGTA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1197 CAGATGCCTTACACCACGATGTGCATCAAGGAATGCCTCCGCCTCTACGCACCGGTAGTA 1256

Qy       1141 AACATATCCCGGTTACTCGACAAACCCATCACCTTTCCAGATGGACGCTCCTTACCTGCA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1257 AACATATCCCGGTTACTCGACAAACCCATCACCTTTCCAGATGGACGCTCCTTACCTGCA 1316

Qy       1201 GGAATAACTGTGTTTATCAATATTTGGGCTCTTCACCACAACCCCTATTTCTGGGAAGAC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1317 GGAATAACTGTGTTTATCAATATTTGGGCTCTTCACCACAACCCCTATTTCTGGGAAGAC 1376

Qy       1261 CCTCAGGTCTTTAACCCCTTGAGATTCTCCAGGGAAAATTCTGAAAAAATACATCCCTAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1377 CCTCAGGTCTTTAACCCCTTGAGATTCTCCAGGGAAAATTCTGAAAAAATACATCCCTAT 1436

Qy       1321 GCCTTCATACCATTCTCAGCTGGATTAAGGAACTGCATTGGGCAGCATTTTGCCATAATT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1437 GCCTTCATACCATTCTCAGCTGGATTAAGGAACTGCATTGGGCAGCATTTTGCCATAATT 1496

Qy       1381 GAGTGTAAAGTGGCAGTGGCATTAACTCTGCTCCGCTTCAAGCTGGCTCCAGACCACTCA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1497 GAGTGTAAAGTGGCAGTGGCATTAACTCTGCTCCGCTTCAAGCTGGCTCCAGACCACTCA 1556

Qy       1441 AGGCCTCCCCAGCCTGTTCGTCAAGTTGTCCTCAAGTCCAAGAATGGAATCCATGTGTTT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1557 AGGCCTCCCCAGCCTGTTCGTCAAGTTGTCCTCAAGTCCAAGAATGGAATCCATGTGTTT 1616

Qy       1501 GCAAAAAAAGTTTGCTAA 1518
              ||||||||||||||||||
Db       1617 GCAAAAAAAGTTTGCTAA 1634
```

RESULT 2
ABK33550
ID ABK33550 standard; cDNA; 2020 BP.
XX
AC ABK33550;
XX
DT 08-MAY-2002 (first entry)
XX
DE cDNA encoding human PRO protein, Seq ID No 29.
XX
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200208288-A2.
XX
PD 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US21066.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220585P.
PR 25-JUL-2000; 2000US-220605P.
PR 25-JUL-2000; 2000US-220607P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220638P.
PR 25-JUL-2000; 2000US-220664P.
PR 25-JUL-2000; 2000US-220666P.
PR 26-JUL-2000; 2000US-220893P.
PR 28-JUL-2000; 2000WO-US20710.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 15-SEP-2000; 2000US-000000P.
PR 10-NOV-2000; 2000WO-US30873.
PR 28-NOV-2000; 2000US-253646P.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001WO-US17092.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2002-172001/22.
DR P-PSDB; AAU83606.
XX
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumours
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT tumour or liver tumour -
XX
PS Claim 2; Figure 29; 359pp; English.
XX
CC The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human
CC PRO protein coding sequences of the invention.
XX
SQ Sequence 2020 BP; 573 A; 489 C; 409 G; 549 T; 0 other;

Query Match 99.9%; Score 1516.4; DB 24; Length 2020;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1517; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 ATGGAGCCCTCCTGGCTTCAGGAACTCATGGCTCACCCCTTCTTGCTGCTGATCCTCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 ATGGAGCCCTCCTGGCTTCAGGAACTCATGGCTCACCCCTTCTTGCTGCTGATCCTCCTC 176

Qy         61 TGCATGTCTCTGCTGCTGTTTCAGGTAATCAGGTTGTACCAGAGGAGGAGATGGATGATC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        177 TGCATGTCTCTGCTGCTGTTTCAGGTAATCAGGTTGTACCAGAGGAGGAGATGGATGATC 236

Qy        121 AGAGCCCTGCACCTGTTTCCTGCACCCCCTGCCCACTGGTTCTATGGCCACAAGGAGTTT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 AGAGCCCTGCACCTGTTTCCTGCACCCCCTGCCCACTGGTTCTATGGCCACAAGGAGTTT 296

Qy        181 TACCCAGTAAAGGAGTTTGAGGTGTATCATAAGCTGATGGAAAAATACCCATGTGCTGTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 TACCCAGTAAAGGAGTTTGAGGTGTATCATAAGCTGATGGAAAAATACCCATGTGCTGTT 356

Qy        241 CCCTTGTGGGTTGGACCCTTTACGATGTTCTTCAGTGTCCATGACCCAGACTATGCCAAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 CCCTTGTGGGTTGGACCCTTTACGATGTTCTTCAGTGTCCATGACCCAGACTATGCCAAG 416

Qy        301 ATTCTCCTGAAAAGACAAGATCCCAAAAGTGCTGTTAGCCACAAAATCCTTGAATCCTGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 ATTCTCCTGAAAAGACAAGATCCCAAAAGTGCTGTTAGCCACAAAATCCTTGAATCCTGG 476

Qy        361 GTTGGTCGAGGACTTGTGACCCTGGATGGTTCTAAATGGAAAAAGCACCGCCAGATTGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 GTTGGTCGAGGACTTGTGACCCTGGATGGTTCTAAATGGAAAAAGCACCGCCAGATTGTG 536

Qy        421 AAACCTGGCTTCAACATCAGCATTCTGAAAATATTCATCACCATGATGTCTGAGAGTGTT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 AAACCTGGCTTCAACATCAGCATTCTGAAAATATTCATCACCATGATGTCTGAGAGTGTT 596

Qy        481 CGGATGATGCTGAACAAATGGGAGGAACGCATTGCCCAAAACTCACGTCTGGAGCTCTTT 540
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        597 CGGATGATGCTGAACAAATGGGAGGAACACATTGCCCAAAACTCACGTCTGGAGCTCTTT 656
```